



1/23

SEQUENCE LISTING

<110> Yoshihiro OHMIYA, EMIKO ASHIDAKA and Seiji ITO

<120> Secreted or membrane-binding chimeric protein

<130> 200521/US

<160> 10

<170> PatentIn version 3.1

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<212> DNA

<213> Artificial Sequence

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<223> fused gene consisting of Vargula Luciferase, yellow fluorescence protein from Aequorea and a DNA coding for spacer peptide

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<222> (1)..(2388)

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cca aca gtt cca act tct tgt gaa gct aaa gaa gga gaa tgt ata gat 144

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acc aga tgc gca aca tgt aaa cga gat ata cta tca gat gga ctg tgt 192  
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Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly			
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Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe			
180	185	190	
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Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile			



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225	230	235	240
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420	425	430	
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Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly			
435	440	445	
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465	470	475	480
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Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val			
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Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys			

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Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu			
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aag taa			2502
Lys			

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&lt;211&gt; 2502

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2502)

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35 40 45	
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Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly	
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Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Ala Gly Asp	
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Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly	
145 150 155 160	
gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc	528
Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr	
165 170 175	

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Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val	
290 295 300	
ctt ttc gac tat gtt gag aca tgc gct gcg ccg gaa acg aga gga acg	960
Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr	
305 310 315 320	

tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga	1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg	
325 330 335	
tat caa ttc cag ggc cca tgc aag gag att ctg atg gcc gca gac tgt	1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys	
340 345 350	
tac tgg aac aca tgg gat gta aag gtt tca cat aga gac gtc gaa tca	1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser	
355 360 365	
tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta	1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val	
370 375 380	
gat ctc att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta	1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val	
385 390 395 400	
tct atc ccg tac agc tct gag aac act tcc ata tac tgg cag gat gga	1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly	
405 410 415	
gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc	1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe	
420 425 430	
aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gga	1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly	
435 440 445	
aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat	1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp	
450 455 460	



ttc	ttt	gac	gca	gaa	gga	gca	tgc	gct	cta	acc	ccc	aac	ccc	cca	gga	1440
Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	
465				470				475					480			
tgt	aca	gag	gaa	cag	aaa	cca	gaa	gct	gag	cga	ctt	tgc	aat	aat	ctc	1488
Cys	Thr	Glu	Glu	Gln	Lys	Pro	Glu	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Leu	
			485					490					495			
ttt	gat	tct	tct	atc	gac	gag	aaa	tgt	aat	gtc	tgc	tac	aag	cct	gac	1536
Phe	Asp	Ser	Ser	Ile	Asp	Glu	Lys	Cys	Asn	Val	Cys	Tyr	Lys	Pro	Asp	
		500					505				510					
cgg	att	gcc	cga	tgt	atg	tac	gag	tat	tgc	ctg	agg	gga	caa	caa	gga	1584
Arg	Ile	Ala	Arg	Cys	Met	Tyr	Glu	Tyr	Cys	Leu	Arg	Gly	Gln	Gln	Gly	
		515				520				525						
ttt	tgt	gac	cat	gct	tgg	gag	ttc	aag	aaa	gaa	tgc	tac	ata	aaa	cat	1632
Phe	Cys	Asp	His	Ala	Trp	Glu	Phe	Lys	Lys	Glu	Cys	Tyr	Ile	Lys	His	
530					535				540							
gga	gac	act	cta	gaa	gta	cca	cct	gaa	tgt	caa	gga	tcc	ctg	gtt	ggc	1680
Gly	Asp	Thr	Leu	Glu	Val	Pro	Pro	Glu	Cys	Gln	Gly	Ser	Leu	Val	Gly	
545				550				555				560				
caa	ctt	ccg	ggc	cga	ctt	ccg	ggc	ccc	ggt	gaa	gcc	ccc	gaa	ccg	ctt	1728
Gln	Leu	Pro	Gly	Arg	Leu	Pro	Gly	Pro	Gly	Glu	Ala	Pro	Glu	Pro	Leu	
			565				570					575				
ctg	cag	ctg	ttt	ctg	ctc	aat	ctc	ccc	cac	ctc	ctc	cag	gcc	ggg	ctc	1776
Leu	Gln	Leu	Phe	Leu	Leu	Asn	Leu	Pro	His	Leu	Leu	Gln	Ala	Gly	Leu	
		580					585				590					
tgt	gga	tcc	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	1824
Cys	Gly	Ser	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	
	595					600				605						

atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val 610 615 620	1872
tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys 625 630 635 640	1920
ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val 645 650 655	1968
acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His 660 665 670	2016
atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val 675 680 685	2064
cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg 690 695 700	2112
gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu 705 710 715 720	2160
aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu 725 730 735	2208
gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln 740 745 750	2256

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 2304  
 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp

755

760

765

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 2352  
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly

770

775

780

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 2400  
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser

785

790

795

800

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 2448  
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu

805

810

815

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 2496  
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr

820

825

830

aag taa

2502

Lys

&lt;210&gt; 4

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Insertion peptide

&lt;400&gt; 4

Gly Ser Thr Glu Pro Gly Leu Glu Glu Val Gly Glu Ile Glu Gln Lys

1 5 10 15

Gln Leu Gln Lys Arg Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala  
20 25 30

Arg Lys Leu Ala Asn Gln Gly Ser  
35 40

<210> 5

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Insertion peptide

<400> 5

Gly Ser Leu Val Gly Gln Leu Pro Gly Arg Leu Pro Gly Pro Gly Glu  
1 5 10 15

Ala Pro Glu Pro Leu Leu Gln Leu Phe Leu Leu Asn Leu Pro His Leu  
20 25 30

Leu Gln Ala Gly Leu Cys Gly Ser  
35 40

<210> 6

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> primer 1

<400> 6

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53

<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer 2

<400> 7

tgtggatcct tgacattcag gtggtacttc tag

33

<210> 8

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> primer 3

<400> 8

caagcttgcg gccgcaggat ccgtgagcaa gggcgaggag ctgttcac

48

<210> 9

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer 4

<400> 9

taccattgtg ctggatggtg agcaagggcg aggagctg

38

<210> 10

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> partial mammalian sequence

<400> 10

Ser Glu Gln Lys Gln Leu Gln Lys Arg Phe Gly Gly Phe Thr Gly Gly

1

5

10

15